STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: _____10/591,752_____

Source: _____TFWP_____

Date Processed by STIC: · _____09/21/2006_____

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
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Revised 01/10/06
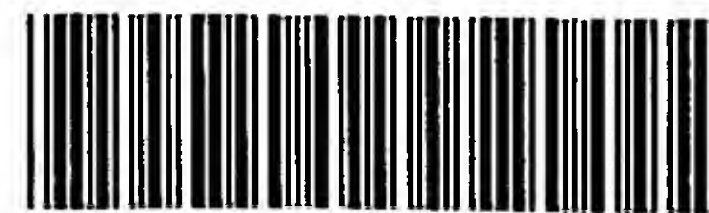
IFWP

RAW SEQUENCE LISTING   DATE: 09/21/2006
PATENT APPLICATION: US/10/591,752   TIME: 11:36:46

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Innovative
      5   Technology for the Earth and Kinki University
W--> 6 <120> TITLE OF INVENTION: Transgenic plants
W--> 7 <130> FILE REFERENCE: C01F1576
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/591,752
C--> 8 <141> CURRENT FILING DATE: 2006-09-01
W--> 8 <160> NUMBER OF SEQ ID: 18

Does Not Comply Corrected Diskette Needed *Cpg-1, 2, 3, 5, 6, 7, 8)*

ERRORED SEQUENCES

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     11 <212> TYPE: PRT
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     35 145   150   155   160
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436 aatctttcta ttgttgtctt ggatcgcggc cgcgctagcg tcgacgatcc ttaggattgg   2160
437 tatattcttt tctatcctgt agtttgtagt ttccctgaat caagccaagt atcacacctc   2220
438 tttctaccca tcctgtatat tgtccccttt gttccgtgtt gaaatagaac cttaatttat   2280
439 tacttatttt tttattaaat tttagatttg ttagtgatta gatattagta ttagacgaga   2340
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441 gcgaatttga cacgacatag gagaagccgc cctttattaa aaattatatt attttaaata   2460
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444 gtctgatagg aaataagata ttcaaataaa taattttata gcgaatgact attcatctat   2640
445 tgtattttca tgcaaatagg gggcaagaaa actctatgga aagatggtgg tttaattcga   2700
446 tgttgtttaa gaaggagttc gaacgcaggt gtgggctaaa taaatcaatg ggcagtcttg   2760
447 gtcctattga aaataccaat gaagatccaa atcgaaaagt gaaaaacatt catagttgga   2820
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454 gtggtagtga gaattacggt gacagttaca tttatagggc cgtttgtggt ggtgaaagtc   3240
455 gaaatagtag tgaaaacgag ggttccagta gacgaactcg cacgaagggc agtgatttaa   3300
456 ctataagaga aagttctaat gatctcgacc tgcaggcatg caagcttggc gtaatcatgg   3360
457 tcatagctgt ttcctgtgtg aaattgttat ccgctcacaa ttccacacaa catacgagcc   3420
458 ggaagcataa agtgtaaagc ctggggtgcc taatgagtga gctaactcac attaattgcg   3480  3540
E--> 459 **ttgcgctcac tgcccgcttt ccagtcggga aacctgtcgt gccagctgca ttaatgaatc**   (3504) 3540
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463 caaaaggcca ggaaccgtaa aaaggccgcg ttgctggcgt ttttccatag gctccgcccc   3780
464 cctgacgagc atcacaaaaa tcgacgctca agtcagaggt ggcgaaaccc gacaggacta   3840
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471 aggacagtat ttggtatctg cgctctgctg aagccagtta ccttcggaaa aagagttggt   4260
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474 gacgctcagt ggaacgaaaa ctcacgttaa gggattttgg tcatgagatt atcaaaaagg   4440
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477 tgtctatttc gttcatccat agttgcctga ctccccgtcg tgtagataac tacgatacgg   4620
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484 ttggccccag tgttatcact catggttatg gcagcactgc ataattctct tactgtcatg   5040
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492 aaaaataaac aaataggggt tccgcgcaca tttccccgaa aagtgccacc tgacgtctaa   5520
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495 <210> SEQ ID NO: 15
496 <211> LENGTH: 1434
497 <212> TYPE: DNA
498 <213> ORGANISM: Nicotiana tabacum
499 <223> OTHER INFORMATION: rbcL
500 <400> SEQUENCE: 15
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503 cgagtaactc ctcaacctgg agttccacct gaagaagcag gggccgcggt agctgccgaa    180
504 tcttctactg gtacatggac aactgtatgg accgatggac ttaccagcct tgatcgttac    240
505 aaagggcgat gctaccgcat cgagcgtgtt gttggagaaa aagatcaata tattgcttat    300
506 gtagcttacc ctttagacct ttttgaagaa ggttctgtta ccaacatgtt tacttccatt    360
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511 aaagatgatg agaacgtgaa ctcacaacca tttatgcgtt ggagagatcg tttcttattt   660
512 tgtgccgaag cactttataa agcacaggct gaaacaggtg aaatcaaagg gcattacttg   720
513 aatgctactg caggtacatg cgaagaaatg atcaaaagag ctgtatttgc tagagaattg   780
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521 cagttcggtg gaggaacttt aggacatcct tgcggtaatg cgccaggtgc cgtagctaat   1260
522 cgagtagctc tagaagcatg tgtaaaagct cgtaatgaag gacgtgatct tgctcaggaa   1320
523 ggtaatgaaa ttattcgcga ggcttgcaaa tggagcccgg aactagctgc tgcttgtgaa   1380
524 gtatggaaag agatcgtatt taattttgca gcagtggacg ttttggataa gtaa         1434
525 <210> SEQ ID NO: 16
526 <211> LENGTH: 705
527 <212> TYPE: DNA
528 <213> ORGANISM: Nicotiana tabacum
529 <223> OTHER INFORMATION: accD
530 <400> SEQUENCE: 16
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533 atcaatgggc agtcttggtc ctattgaaaa taccaatgaa gatccaaatc gaaaagtgaa    180
534 aaacattcat agttggagga atcgtgacaa ttctagttgc agtaatgttg attatttatt    240
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536 tggagacagt tattccatct attttgatat tgaaaatcat atttttgaga ttgacaacga    360
537 tcattctttt ctgagtgaac tagaaagttc tttttatagt tatcgaaact cgaattatcg    420
538 gaataatgga tttaggggcg aagatcccta ctataattct tacatgtatg atactcaata    480
539 tagttggaat aatcacatta atagttgcat tgatagttat cttcagtctc aaatctgtat    540
540 agatacttcc attataagtg gtagtgagaa ttacggtgac agttacattt atagggccgt    600
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544 <211> LENGTH: 21
545 <212> TYPE: DNA
546 <213> ORGANISM: Artificial sequence
547 <223> OTHER INFORMATION: polylinker
548 <400> SEQUENCE: 17
549 cgcggccgcg ctagcgtcga c                                                21
551 <210> SEQ ID NO: 18
552 <211> LENGTH: 7
553 <212> TYPE: DNA
554 <213> ORGANISM: Artificial sequence
555 <223> OTHER INFORMATION: Shine-Dalgarno Sequence
556 <400> SEQUENCE: 18
557 aggaggu                                                                 7
558 ??
560 ??
562 ??
564 ??
571 1/14
```

VERIFICATION SUMMARY   DATE: 09/21/2006
PATENT APPLICATION: **US/10/591,752**   TIME: 11:36:47

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\09212006\J591752.raw**

```
L:6 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:9 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <220> field identifier
L:13 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:15 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:14
L:43 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:66 M:283 W: Missing Blank Line separator, <220> field identifier
L:66 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:68 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:67
L:91 M:283 W: Missing Blank Line separator, <220> field identifier
L:91 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:93 M:283 W: Missing Blank Line separator, <400> field identifier
L:93 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:92
L:140 M:283 W: Missing Blank Line separator, <220> field identifier
L:140 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:142 M:283 W: Missing Blank Line separator, <400> field identifier
L:142 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:141
L:164 M:283 W: Missing Blank Line separator, <220> field identifier
L:164 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:165 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:166
L:219 M:283 W: Missing Blank Line separator, <220> field identifier
L:219 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:220 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:221 M:283 W: Missing Blank Line separator, <400> field identifier
L:250 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:250 M:283 W: Missing Blank Line separator, <400> field identifier
L:259 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8
L:259 M:283 W: Missing Blank Line separator, <400> field identifier
L:268 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9
L:268 M:283 W: Missing Blank Line separator, <400> field identifier
L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:288 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10
L:288 M:283 W: Missing Blank Line separator, <400> field identifier
L:370 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:371 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:378 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:12
L:378 M:283 W: Missing Blank Line separator, <400> field identifier
L:387 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
L:387 M:283 W: Missing Blank Line separator, <400> field identifier
```

VERIFICATION SUMMARY   DATE: 09/21/2006
PATENT APPLICATION: **US/10/591,752**   TIME: 11:36:47

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\09212006\J591752.raw**

```
L:399 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:400 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14
L:400 M:283 W: Missing Blank Line separator, <400> field identifier
L:459 M:254 E: No. of Bases conflict, LENGTH:Input:3504 Counted:3540 SEQ:14
L:500 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:500 M:283 W: Missing Blank Line separator, <400> field identifier
L:530 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:530 M:283 W: Missing Blank Line separator, <400> field identifier
L:547 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:548 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:548 M:283 W: Missing Blank Line separator, <400> field identifier
L:555 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:556 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:18
L:556 M:283 W: Missing Blank Line separator, <400> field identifier
L:558 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:560 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:562 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:562 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:564 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:571 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:571 M:254 E: No. of Bases conflict, LENGTH:Input:14 Counted:8 SEQ:18
L:571 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:571 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:8 SEQ:18
```